abundant resources during summer but also survive winter. How aphids have evolved this ability to switch between parthenogenesis and sexual meiosis is unknown. To arrive at a mechanistic explanation for this developmental plasticity, I determined meiosis gene activity in sexuals and asexuals. I first identified homologs of a core set of meiosis genes from the pea aphid genome. Next, I tested the expression of these core meiosis genes by PCR spanning across at least one intron from cDNA isolated from asexual and sexual ovaries. Surprisingly, meiosis specific genes (e.g., *Spo11*, *Msh4*, *Msh5*, *Hop2* and *Mnd1*) are expressed in asexual ovaries. Additionally, the Spo11 PCR product contained intronic sequence, thus representing unspliced mRNA. Future experiments looking at the quantities and localizations of mRNA and protein will help to distinguish among several possible explanations for these results. Further molecular characterization of this phenotypic plasticity will be helpful in understanding how multiple interacting pathways can evolve to create alternate developmental phenotypes.

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Program/Abstract # 88
Evolution of the *Drosophila* larval trichome pattern through *cis*-regulatory mutations at an enhancer of a single gene
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What is the nature of the genetic and developmental events responsible for morphological change? Although central to evolutionary biology, in only a handful of cases has this question been answered in terms of identifying and confirming genetically the actual genes responsible for the evolution of a particular morphological difference. In fewer still have the relevant specific changes in genes been identified and understood in terms of their effects on development. Previous work has shown that expression of the gene *shavenbaby* (*svb*), a gene required for the development of larval trichomes in *Drosophila*, is controlled by at least three discrete *cis*-regulatory enhancers. It has further been shown that a loss of larval trichomes in the lineage leading to *Drosophila sechellia* is due to recent evolutionary changes in *svb* occurring in all three of these enhancers. Here we describe recent progress in delimiting and dissecting one of these enhancers–the one required for lateral trichomes–with the goal of identifying the specific nucleotide changes responsible for the absence of lateral trichomes in the larvae of *D. sechellia*.

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Program/Abstract # 89
Evolution of the *Drosophila* folded gastrulation gene
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In the fruit fly *Drosophila melanogaster* the prospective mesodermal and endodermal cells are internalised through a series of highly co-ordinated cell shape changes during gastrulation. The *folded gastrulation* gene (*fog*) is known to provide a signal that controls the initial steps of this process. Under the control of *fog* signal cells first flatten and then constrict their apical surface thereby initiating their inward movement from the outer epithelial cell layer of the blastoderm. Despite the importance of *fog* in initiating these cell shape changes the *fog* gene was thought to be unique to *Drosophila*. However, the *fog* signal feeds into a conserved pathway involving the well characterised Rho GTPase signalling cascade. This pathway ultimately leads to activation of the molecular motor myosin that drives the changes in cell shape. This raises interesting questions about the evolutionary origin of the novel *fog* gene, its mechanism of action and how it relates to components of this pathway in other organisms. To address the question of *fog*'s evolutionary origins we have searched for *fog* homologs in closely related species of *Drosophila* and used these to then search for more distant homologs in other insects. We will present the results of our analysis including identified homolgs in twelve species of *Drosophila* and our preliminary findings of *fog* homologs in other insect species. We are also beginning an in depth analysis of the expression of these *fog* homologs and progress from this expression analysis will also be included.

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Program/Abstract # 90
Temperature-tolerance and protein stability assays of *Drosophila melanogaster*
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Numerous mutants of the fruit fly, *Drosophila melanogaster*, have been generated and the genetic basis of their phenotypes has been extensively studied. We investigated the temperature-tolerance of adults of the wild type (wt), eye color mutant white (w), sepia (se), scarlet (st) and brown (bw), body color mutant ebony (e), wing mutant vestigial (vg), and circadian rhythm mutant period (per) and timeless (tim) at 4 °C, 18 °C and 37 °C. The numbers of mating males and females were kept constant and the emergence and the number of larvae and pupae were closely monitored. As expected, the flies survived and reproduced well at 18 °C, with st having the highest reproductive success. The larval and pupal stages of wt were shorter than those of st and tim at this temperature. At 37 °C, flies were prone to dehydration and fermentation by yeast present in the culture medium. We found that at 37 °C, e and tim had a higher survival rate than wt, w, bw, se, st and vg, and e had a higher survival rate than wt at 4 °C. When kept for three days at 4 °C, flies failed to develop, but wt and se were able to recover when moved into 18 °C. We are also investigating if the differences in survival, mating success, and the duration of the larval and pupal stages at each temperature tested correspond to the differences in protein stability of the different types of flies. We are in the process of extracting proteins from each type of adult flies for analyzing protein concentrations by the BCA assay. The protein extracts will be aliquoted and we will use two methods to measure protein stability.

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Program/Abstract # 91
Analyzing the role of CtBP in *Drosophila* eye development
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Eye specification requires precisely coordinated regulation of many genes. One of these genes, *atonal* (*ato*), is essential for specification of